SEQUENCE LISTING

<110> IKADAI, Hiromi et al.

<120> GENE ENCODING PROTEIN FROM MEROZOITE OF BABESIA CABALLI, RECOMBINANT
PROTEIN OBTAINED WITH SAID GENE AND USE THEREOF

<130> 0020-4843P

<140> 09/807,459
<141> 2001-04-13

<160> 2

<170> PatentIn version 3.0

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                                           1   5

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Val Gly Asp Val Thr Lys Thr Leu Leu Ala Ala Ser Glu Ser Val Asp
            10   15   20

tca gct gcc aat gcc tat atg atc aac agt gac atg agc gat tac ttg   152
Ser Ala Ala Asn Ala Tyr Met Ile Asn Ser Asp Met Ser Asp Tyr Leu
            25   30   35

tcg gct gtg tct gac aac ttc gcc gag cgc att tgc agt cag gtc cct   200
Ser Ala Val Ser Asp Asn Phe Ala Glu Arg Ile Cys Ser Gln Val Pro
        40   45   50

aag ggg agt aac tgc agt gct tcc gtt agc gca tac atg agt cgc tgc   248
Lys Gly Ser Asn Cys Ser Ala Ser Val Ser Ala Tyr Met Ser Arg Cys
55   60   65   70

gct aaa cag gac tgc ctg act ctc caa agt ctt aag tac cct ctt gag   296
Ala Lys Gln Asp Cys Leu Thr Leu Gln Ser Leu Lys Tyr Pro Leu Glu
                75   80   85

gct aag tac caa ccg ctg acc ctt cct gac ccc tac cag ttg gag gcc   344
Ala Lys Tyr Gln Pro Leu Thr Leu Pro Asp Pro Tyr Gln Leu Glu Ala
            90   95   100

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gca ttt ata ctc ttc aag gag agt gac gct aat ccg gcc aat agc act        392
Ala Phe Ile Leu Phe Lys Glu Ser Asp Ala Asn Pro Ala Asn Ser Thr
        105             110             115

gag aag cgc ttc tgg atg cgt ttc aga agg ggc aag aac cac agt tac        440
Glu Lys Arg Phe Trp Met Arg Phe Arg Arg Gly Lys Asn His Ser Tyr
        120             125             130

ttc cac gac tta gtc ttc aat ctg ctg gag aag aac gtg act cgc gac        488
Phe His Asp Leu Val Phe Asn Leu Leu Glu Lys Asn Val Thr Arg Asp
135             140             145             150

gcg gat gct act gac att gag aac ttt gcg tcc agg tac ctg tac atg        536
Ala Asp Ala Thr Asp Ile Glu Asn Phe Ala Ser Arg Tyr Leu Tyr Met
                155             160             165

gcc acg ctt tac tac aag acg tac acg aat gtt gat gag ttc ggt gct        584
Ala Thr Leu Tyr Tyr Lys Thr Tyr Thr Asn Val Asp Glu Phe Gly Ala
                170             175             180

agc ttc ttt aac aag ttg tct ttc act act ggg ttg ttc ggc tgg ggc        632
Ser Phe Phe Asn Lys Leu Ser Phe Thr Thr Gly Leu Phe Gly Trp Gly
                185             190             195

atc aag agg gca ctt aag cag att att cgc tct aac ctg ccc ctt gac        680
Ile Lys Arg Ala Leu Lys Gln Ile Ile Arg Ser Asn Leu Pro Leu Asp
        200             205             210

atc ggg aca gaa cac agc gtc agt cgc ctg cag cac att acg agc agt        728
Ile Gly Thr Glu His Ser Val Ser Arg Leu Gln His Ile Thr Ser Ser
215             220             225             230

tac aag gat tac atg gat acg cag att cct gca ctg ccc aag ttt gcg        776
Tyr Lys Asp Tyr Met Asp Thr Gln Ile Pro Ala Leu Pro Lys Phe Ala
                235             240             245

aag cgt ttc tcc ctt atg gta gtg cag agg ctg ctg gcc acc gtg gct        824
Lys Arg Phe Ser Leu Met Val Val Gln Arg Leu Leu Ala Thr Val Ala
                250             255             260

ggt tac gtc gac acc ccg tgg tat aag aag tgg tac atg aag ctg aag        872
Gly Tyr Val Asp Thr Pro Trp Tyr Lys Lys Trp Tyr Met Lys Leu Lys
                265             270             275

aac ttt atg gtg aac agg gtg ttc att cct aca aag aag ttc ttc aat        920
Asn Phe Met Val Asn Arg Val Phe Ile Pro Thr Lys Lys Phe Phe Asn
        280             285             290

aag gaa att cgt gag cct agt aag gca tta aaa gaa aag gtg tca acc        968
Lys Glu Ile Arg Glu Pro Ser Lys Ala Leu Lys Glu Lys Val Ser Thr
295             300             305             310

gac acc aag gat tta ttc gag aac aaa att ggg cag ggt act gtg gac       1016
Asp Thr Lys Asp Leu Phe Glu Asn Lys Ile Gly Gln Gly Thr Val Asp
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2

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ttc ttc aat aag gaa att cgt gac cct agt aag gca tta aaa gaa aaa      1064
Phe Phe Asn Lys Glu Ile Arg Asp Pro Ser Lys Ala Leu Lys Glu Lys
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gtg tca aac gac gcc aag gat tta ttc gag aac aaa att ggg cag ggt      1112
Val Ser Asn Asp Ala Lys Asp Leu Phe Glu Asn Lys Ile Gly Gln Gly
            345                 350                 355

act gtg gac ttc atc aat aac gaa att cgt gac cct agt aag gca tta      1160
Thr Val Asp Phe Ile Asn Asn Glu Ile Arg Asp Pro Ser Lys Ala Leu
    360                 365                 370

ata aga aaa gtg tca acg ggg gcc gag gat tta ttc gag aac aaa att      1208
Ile Arg Lys Val Ser Thr Gly Ala Glu Asp Leu Phe Glu Asn Lys Ile
375                 380                 385                 390

ggg cag ggt act gtg gac ttc atc aat aac gaa att cgt gac cct agt      1256
Gly Gln Gly Thr Val Asp Phe Ile Asn Asn Glu Ile Arg Asp Pro Ser
                395                 400                 405

aag gca tta ata aga aaa gtg tac acc gag gcc gat gat tta ttc gag      1304
Lys Ala Leu Ile Arg Lys Val Tyr Thr Glu Ala Asp Asp Leu Phe Glu
                410                 415                 420

aac aaa att ggg cag ggt act gtg gac ttc atc aat aag gaa att cgt      1352
Asn Lys Ile Gly Gln Gly Thr Val Asp Phe Ile Asn Lys Glu Ile Arg
            425                 430                 435

gac cct agt aag gca tta ata aga aaa gtg tct acc gag gcc gat aat      1400
Asp Pro Ser Lys Ala Leu Ile Arg Lys Val Ser Thr Glu Ala Asp Asn
    440                 445                 450

tta ttg gag aaa taggttgcga agcccctgag gaagcaccgc aagggcaacg         1452
Leu Leu Glu Lys
455

ttagtgacag cggggaatct gaggaaattt cggctgtggg tgaatctttg gaatccgaca    1512

acgaaatgaa gacccaggag tcaatgaact cggagagtgc ttctaccgaa ctcccttctg    1572

aggagtccga ggaagagtcg gctgctatgg ttattcagca gcccaccctg gaggaggcca    1632

gccagatcgc attgcctgct gaagaagaca gctcagagtt gcaggaaacc tccgacaact    1692

atgaagcctc tctctagtca cctttgacgt ccatcgcact gctcggagaa tataaaacgc    1752

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3

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            20   25   30

Asp Met Ser Asp Tyr Leu Ser Ala Val Ser Asp Asn Phe Ala Glu Arg
        35   40   45

Ile Cys Ser Gln Val Pro Lys Gly Ser Asn Cys Ser Ala Ser Val Ser
    50   55   60

Ala Tyr Met Ser Arg Cys Ala Lys Gln Asp Cys Leu Thr Leu Gln Ser
65   70   75   80

Leu Lys Tyr Pro Leu Glu Ala Lys Tyr Gln Pro Leu Thr Leu Pro Asp
            85   90   95

Pro Tyr Gln Leu Glu Ala Ala Phe Ile Leu Phe Lys Glu Ser Asp Ala
            100   105   110

Asn Pro Ala Asn Ser Thr Glu Lys Arg Phe Trp Met Arg Phe Arg Arg
        115   120   125

Gly Lys Asn His Ser Tyr Phe His Asp Leu Val Phe Asn Leu Leu Glu
    130   135   140

Lys Asn Val Thr Arg Asp Ala Asp Ala Thr Asp Ile Glu Asn Phe Ala
145   150   155   160

Ser Arg Tyr Leu Tyr Met Ala Thr Leu Tyr Tyr Lys Thr Tyr Thr Asn
                165   170   175

Val Asp Glu Phe Gly Ala Ser Phe Phe Asn Lys Leu Ser Phe Thr Thr
            180   185   190

Gly Leu Phe Gly Trp Gly Ile Lys Arg Ala Leu Lys Gln Ile Ile Arg
        195   200   205

Ser Asn Leu Pro Leu Asp Ile Gly Thr Glu His Ser Val Ser Arg Leu
    210   215   220

4

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Gln His Ile Thr Ser Ser Tyr Lys Asp Tyr Met Asp Thr Gln Ile Pro
225                 230                 235                 240

Ala Leu Pro Lys Phe Ala Lys Arg Phe Ser Leu Met Val Val Gln Arg
                245                 250                 255

Leu Leu Ala Thr Val Ala Gly Tyr Val Asp Thr Pro Trp Tyr Lys Lys
                260                 265                 270

Trp Tyr Met Lys Leu Lys Asn Phe Met Val Asn Arg Val Phe Ile Pro
                275                 280                 285

Thr Lys Lys Phe Phe Asn Lys Glu Ile Arg Glu Pro Ser Lys Ala Leu
                290                 295                 300

Lys Glu Lys Val Ser Thr Asp Thr Lys Asp Leu Phe Glu Asn Lys Ile
305                 310                 315                 320

Gly Gln Gly Thr Val Asp Phe Phe Asn Lys Glu Ile Arg Asp Pro Ser
                325                 330                 335

Lys Ala Leu Lys Glu Lys Val Ser Asn Asp Ala Lys Asp Leu Phe Glu
                340                 345                 350

Asn Lys Ile Gly Gln Gly Thr Val Asp Phe Ile Asn Asn Glu Ile Arg
                355                 360                 365

Asp Pro Ser Lys Ala Leu Ile Arg Lys Val Ser Thr Gly Ala Glu Asp
    370                 375                 380

Leu Phe Glu Asn Lys Ile Gly Gln Gly Thr Val Asp Phe Ile Asn Asn
385                 390                 395                 400

Glu Ile Arg Asp Pro Ser Lys Ala Leu Ile Arg Lys Val Tyr Thr Glu
                405                 410                 415

Ala Asp Asp Leu Phe Glu Asn Lys Ile Gly Gln Gly Thr Val Asp Phe
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Ile Asn Lys Glu Ile Arg Asp Pro Ser Lys Ala Leu Ile Arg Lys Val
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